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Amendments to the Claims:

1. (previously presented) A method of reducing pathogenicity to a plant of a fungus that produces fumonisin, comprising:

a) stably integrating into the genome of a plant cell a first nucleotide sequence operably linked to a promoter active in said plant cell, wherein said first nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32 and encodes a polypeptide having amine oxidase activity;

b) optionally stably integrating into the genome of said plant cell a second nucleotide sequence operably linked to a promoter active in said plant cell, wherein said second nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 12 or 14 and encodes a polypeptide having fumonisin esterase activity;

c) stably integrating into the genome of said plant cell a nucleotide sequence operably linked to a promoter active in said plant cell, wherein said nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, and encodes a polypeptide having fumonisin detoxification activity; and

d) regenerating a transformed plant from said plant cell,

whereby the pathogenicity of said fungus to said transformed plant is reduced in comparison to the pathogenicity of said fungus to a plant that has not been transformed.

2. (previously presented) The method of claim 1, wherein said second nucleotide sequence comprises the sequence set forth in SEQ ID NO: 12 or 14.

3. (previously presented) The method of claim 1, wherein the nucleotide sequence of step (c) comprises the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

4. (previously presented) The method of claim 1, wherein said first nucleotide sequence comprises the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32.

5. (previously presented) The method of claim 1, wherein said plant cell is a cell from a monocot.

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6. (previously presented) The method of claim 5, wherein said monocot is maize.
7. (previously presented) The method of claim 1, wherein said plant cell is a cell from a dicot.
8. (previously presented) The method of claim 1, wherein the promoter of step (a) is an inducible promoter.
9. (previously presented) The method of claim 1, wherein the promoter of step (a) is a tissue-preferred promoter.
10. (previously presented) A plant having stably integrated into its genome:
 - a) a first nucleotide sequence operably linked to a promoter active in said plant, wherein said first nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32 and encodes a polypeptide having amine oxidase activity;
 - b) optionally, a second nucleotide sequence operably linked to a promoter active in said plant, wherein said second nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 12 or 14 and encodes a polypeptide having fumonisin esterase activity; and,
 - c) a nucleotide sequence operably linked to a promoter active in said plant, wherein said nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, and encodes a polypeptide having fumonisin detoxification activity.
11. (previously presented) The plant of claim 10, wherein said second nucleotide sequence is set forth in SEQ ID NO: 12 or 14.

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12. (previously presented) The plant of claim 10, wherein said first nucleotide sequence encodes a polypeptide having the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33.

13. (previously presented) The plant of claim 10, wherein said first nucleotide sequence comprises the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32.

14. (previously presented) The plant of claim 10, wherein said plant is a monocot.

15. (previously presented) The plant of claim 14, wherein said monocot is maize.

16. (previously presented) The plant of claim 10, wherein said plant is a dicot.

17. (previously presented) Transformed seed of the plant of claim 10.

18. (previously presented) A plant cell having stably integrated into its genome:
a) a first nucleotide sequence operably linked to a promoter active in said plant cell, wherein said first nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32 and encodes a polypeptide having amine oxidase activity;

b) optionally, a second nucleotide sequence operably linked to a promoter active in said plant cell, wherein said second nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 12 or 14 and encodes a polypeptide having fumonisin esterase activity; and,

c) a nucleotide sequence operably linked to a promoter active in said plant cell, wherein said nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10 and encodes a polypeptide having fumonisin detoxification activity.

19. (previously presented) A method of reducing pathogenicity to a plant of a fungus that produces fumonisin, comprising stably integrating into the genome of a plant cell:

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- a) a first nucleotide sequence operably linked to a promoter active in said plant cell, wherein said first nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33 and having amine oxidase activity;
 - b) optionally, a second nucleotide sequence operably linked to a promoter active in said plant cell, wherein said second nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 13 or 15 and having fumonisin esterase activity;
 - c) a nucleotide sequence operably linked to a promoter active in said plant cell, wherein said nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 3, 5, 8, or 11, and having fumonisin detoxification activity; and
 - d) regenerating a transformed plant from said plant cell,
- whereby the pathogenicity of said fungus to said transformed plant is reduced in comparison to the pathogenicity of said fungus to a plant that has not been transformed.

20. (previously presented) A plant having stably integrated into its genome

- a) a first nucleotide sequence operably linked to a promoter active in a plant cell, wherein said first nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33 and having amine oxidase activity;
- b) optionally, a second nucleotide sequence operably linked to a promoter active in a plant cell, wherein said second nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 13 or 15 and having fumonisin esterase activity; and,
- c) a nucleotide sequence operably linked to a promoter active in a plant cell, wherein said nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 3, 5, 8, or 11 and having fumonisin detoxification activity.

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21. (previously presented) The method of claim 1, wherein the nucleotide sequence of step (c) has at least 98% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

22. (previously presented) The method of claim 1, wherein the nucleotide sequence of step (c) encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

23. (previously presented) The plant cell of claim 18, wherein said first nucleotide sequence is set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32.

24. (previously presented) The plant of claim 10, wherein the nucleotide sequence of step (c) encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

25. (previously presented) The plant of claim 10, wherein the nucleotide sequence of step (c) is the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

26. (previously presented) The plant cell of claim 18, wherein said first nucleotide sequence has at least 98% sequence identity to the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32, said second nucleotide sequence has at least 98% sequence identity to the sequence set forth in SEQ ID NO: 12 or 14, and the nucleotide sequence of step (c) has at least 98% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

27. (previously presented) The plant cell of claim 18, wherein the nucleotide sequence of step (c) encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

28. (previously presented) The plant cell of claim 18, wherein said first nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33, said second nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 13 or 15, and the nucleotide sequence of step (c) encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 3, 5, 8, or 11.

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29. (currently amended) The method of claim 1, wherein said first nucleotide sequence encodes a polypeptide having the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33, said second nucleotide sequence encodes a polypeptide having the sequence set forth in SEQ ID NO: 13 or 15, and the nucleotide sequence of step (c) encodes a polypeptide having the sequence set forth in SEQ ID NO: 3, 5, 8, or 11.

30. (previously presented) The plant cell of claim 18, wherein said first nucleotide sequence encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33, said second nucleotide sequence encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 13 or 15, and the nucleotide sequence of step (c) encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 3, 5, 8, or 11.

31. (previously presented) The plant cell of claim 18, wherein the nucleotide sequence of step (c) is set forth in SEQ ID NO: 2, 4, 7, or 10.

32. (previously presented) The plant of claim 10, wherein said first nucleotide sequence encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33, said second nucleotide sequence encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 13 or 15, and the nucleotide sequence of step (c) encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 3, 5, 8, or 11.

33. (previously presented) The plant cell of claim 18, wherein said second nucleotide sequence is set forth in SEQ ID NO: 12 or 14.